

Host-specific differences in the contribution of an extended spectrum β -lactamase (ESBL) IncI1 plasmid to intestinal colonisation by *Escherichia coli* O104:H4

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Table S1. Bacterial strains and primers used in this study.

Strain/ plasmid	Genotype/phenotype	Reference
BL211	<i>E. coli</i> O104:H4 Δ stx2AB::Gent ^R ; Tet ^R ; Ctx ^R	5
BL320	BL211 derivative lacking pESBL	This study
pIMF27	Inc1 curing vector, Kan ^R	13

Primers

Gene	Sequence	Reference
<i>Chromosomal markers</i>		
<i>terD</i> (434 bp)	5'-AGTAAAGCAGCTCCGTCAAT-3' 5'-CCGAACAGCATGGCAGTCT-3'	3
<i>rfb</i> _{O104} (351 bp)	5'-TGAAGTATTTTTAGGATGG-3' 5'-AGAACCTCACTCAAATTATG-3'	3
<i>fliC</i> _{H4} (201 bp)	5'-GGCGAAACTGACGGCTGCTG-3' 5'-GCACCAACAGTTACCGCCGC-3'	3
<i>Plasmid-specific markers</i>		
<i>aggR</i> (254 bp) for pAA	5'-GTATACACAAAAGAAGGAAGC-3' 5'-ACAGAATCGTCAGCATCAGC-3'	37
<i>bla</i> _{CTX-M} (593 bp) for pESBL	5'-ATGTGCAGYACCAAGTAARGTKATGGC-3' 5'-TGGGTRAARTARGTSACCAGAAAYAAGCGG-3'	38
<i>alternative bla</i> _{CTX-M} (260 bp)	5'-GCGTGATACCACTTCACCTC-3' 5'-TGAAGTAAGTGACCAGAATC-3'	39

PCR reactions were performed using the QIAGEN Multiplex PCR reagents and the following conditions: 95 °C for 15 min, followed by 25 cycles consisting of 95 °C for 30s, 54 °C for 30s and 72 °C for 1 min, with a final extension step of 72 °C for 5 min. PCR products were analysed by electrophoresis on 2% agarose gels and visualised using ethidium bromide (5 µg/mL) or RedsafeTM.

Table S2. Diarrhoeal status of infant rabbits infected with the different strains of bacteria.

Strain	BL211	BL320
Diarrhoea (%)	18	11
Disease category		
Diarrhoea	0	0
Intestinal disease	3	2
None	14	17
Total number of animals	17	19
P-value* versus BL211	-	NS

*Fisher's exact test

Table S3. Recovery of *E. coli* O104 strains in weaned sheep at 4 days post infection.

Strain	Animal No.	cfu/g tissue sample [\log_{10}]				RAJ ^a
		ileum	caecum	colon	rectum	
BL211	1	0 ^b	2.5	2.8	0	0
	2	0	1 ^c	0	1	1
	3	5.0	4.2	3.9	1	1
BL320	1	0	2.3	2.3	2.8	1
	2	2.3	1	1	1	2.0
	3	0	1	1	1	2.3

RAJ^a = recto-anal junction

0^b = No colonies were recovered even after enrichment

1^c = Colonies were recovered after enrichment

Figure S1

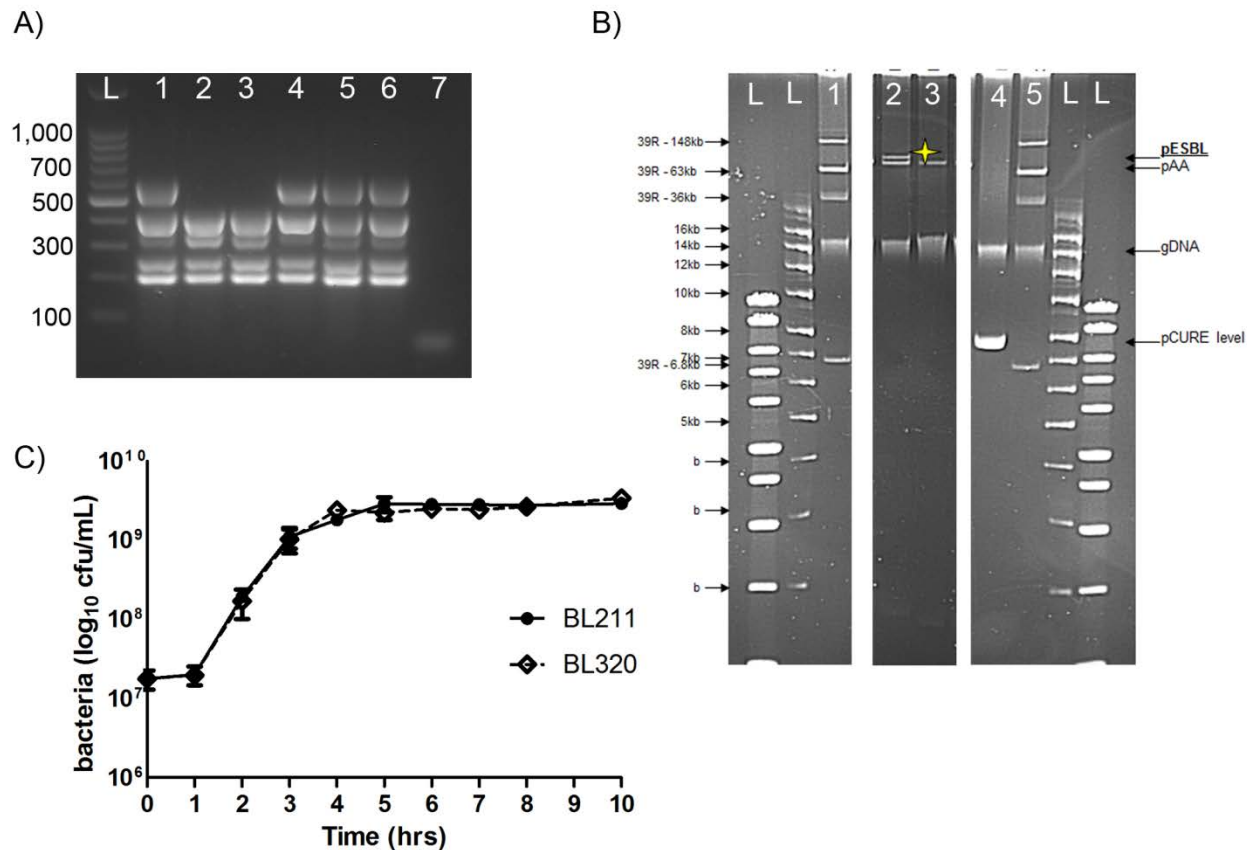


Figure S1. Confirmation of pESBL loss from *E. coli* O104:H4. Multiplex PCR was used to amplify chromosomal (*terD* (434bp), *rfb*_{O104} (351 bp), *fliC* (201 bp) and plasmid-borne (*bla*_{CTX-M} (593 bp), *aggR* (254 bp)) genes (A). Products were visualised on a 2% agarose gel. Lanes: L - 100 bp DNA ladder, 1- parent strain BL211; 2 - pESBL-cured strain BL320; 3 – cefotaxime-susceptible output colony; 4 to 6 – representative cefotaxime-resistant colonies and 7 – negative control (ddH₂O). Plasmid profile of strains (B). Plasmid DNA and visualised on 0.8% agarose gel. Lanes: L-DNA ladders; 1 – *E. coli* 39R reference strain; 2 – wild type strain BL211; 3 – pESBL-cured strain BL320; 4 – pIFM27 plasmid; 5 – *E. coli* 39R reference strain. All lanes are from the same gel but extra lanes have been removed. Yellow star indicates missing band corresponding to pESBL plasmid. Growth of wild-type and pESBL-cured strain in LB media over time (C). Bacterial numbers were determined by serial dilution and plating

on LB agar supplemented with antibiotics. Data represent means \pm standard deviation of 3 biological replicates.

